

Amendments to the Specification

On page 11, amend the paragraph starting on line 15 as follows.

The output array can contain hundreds, thousands, or millions of resulting yeast strains with genetic alterations. In one embodiment, the output array contains between about 1,000 and 25 million resulting yeast strains, and more preferably between about one and about 25 million resulting yeast strains. Because the output array can be produced in such a high-density format, containing millions of yeast strains, the output array can be used to assign gene function to multiple genes simultaneously. The high-density output array also allows for large-scale analysis of genetic and protein interactions, by analyzing the phenotypes of the resulting strains within the output array.

On page 23, amend the paragraph starting on line 23 as follows.

An example of a starting strain that could be used in this embodiment is the *Saccharomyces cerevesiae* strain termed Y2454. The Y2454 strain is characterized by being a *MAT $\alpha$*  mating type with *ura3*, *leu2*, *his3*, and *lys2* mutations, and a *HIS3* gene linked to an *MFA1* promoter. The *ura3*, *leu2*, *his3*, and *lys2* mutations require the strain to be grown in supplemented media to survive. They also carry a *can1* null allele which confers canavanine resistance to the cells. A mutant gene, for example, one of the approximately 5,000 non-lethal mutations found in *Saccharomyces cerevesiae*, is introduced into this strain. The deleted gene is being replaced by a *NAT* gene which confers noureseothricin resistance to these cells.